

B-™

GTTTTTCGG

GATTTGGGAA AGAGGGAAAG

TTTCGTTGGG

ATTTTTAGG

TTGTTTGTTT

TTGTTGTGGT TCGTTGCGGT

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TTTTTTTG

	Figure 2	Ω	Upstream Region of Differential Methylation in Prostate Cancer	n of Differentia	al Methylation	in Prostate Ca	ncer		
	дерарарар	АТААААТААА	ATAAAGCAAT	TTCCTTTCCT	-43 CTAAGCGGCC	TCCACCCTC	TCCCCTGCCC	-42 TGTGAAGCGG	-355
	ATAAAATAAA	ATAAAATA	ATARARIARA ATARARIARA ATARAGTARI TITITITIT TIRAGIGGIT TITATITITI TITITITITI TGIGAAGIGG	TTTTTTTT	TTAAGTGGTT	TTTATTTT	TTTTTTT	TGTGAAGTGG	B-U
	ATAAAATAAA	ATAAAATAAA	ATAAAATAAA ATAAAATAAA ATAAAGTAAT	TTTTTTTT	TTAAGCGGTT	TTTATTTTT	TTTTTTGTTT	TGTGAAGCGG	B-M
			00		138.37	75-45-95-1	GTA-GC (p)	(b)	
	GTGTGCAAGC	GTGTGCAAGC TCCGGGATCG	CAGO	AGGGAATTTC	CCCCGCGAT	Greceges Gecagness	GCCAGTTCGC	CACACT	-275
5	GTGTGTAAGT	TTTGGGATTG		AGGGAATTTT	TTTTTGTGAT	GTTTTGGTGT GTTAGTTTGT GTTTCGGCGC GTTAGTTCGT	GTTAGTTTGT	TGTGTATATT TGCGTATATT	D-G B-G
SUB				+ + + + + + + + + + + + + + + + + + +		) ) ) ) ) (			
STI		CGPS-5		YGGTTTT AGGGAATTTT	TTTTCGC>CG	YS-6 YGGYGY	TTTTCGC>CGPS-6 YGGYGY GTTAGTTYGT TGYGTATATT	TGYGTATATT	
TU			CGPS-11	GGGAATTTT	TTTTCGCGAT	TITICGCGAI GITIYGGCGC>			
TE SHI									
EET	-31 -30				-29			-28	
(Ru	E	CCTCTTCCTG	CCICITCCIG CIGICIGIII	ACTCCCTAGG	ACTCCCTAGG CCCCGCTGGG GACCTGGGAA AGAGGGAAAG GCTTCCCCGG	GACCTGGGAA	AGAGGGAAAG	GCTTCCCCGG	-195
le 2	TTGTTGTGGT	TTTTTTTG	TTGTTTGTTT		ATTTTTAGG TTTTGTTGGG GATTTGGGAA AGAGGGAAAG	GATTTGGGAA	AGAGGGAAAG	GTTTTTTGG B-U	B-U

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B-U B-W CAGCGCCGC CGGGGCTGGG TGGGGTTGGG CGGGGTTGGG -18 -17 -16 TAGTGGTTGT TAGCGGTCGT TGCGGCCGAC GCCCGGGGTG TGTGGTTGAT GTTTGGGGTG TGCGGTCGAC GTTCGGGGTG -22 -21 -20 -19 GGCGCCCTC GGTGTTTTT GGCGTTTTT GGGACTCCAG GGGATTTAG GGGATTTTAG CCAGCTGCGC GGCGACTCCG TIAGITGCGC GGCGATITCG GGTGATTTG -24 -27-26-25 TTAGTTGTGT

< GCTG CAARCCCCAC ATCRCCARCA RCCCCA CGPS-8 SCCARCA GCCCCAACCC < G CCGCTAAAGC CCCTAAAATC CCRCAAAA CGPS-12 <GCG CCRCTAAARC CCCTAAAATC CCRC CGPS-7</pre>

SUBSTITUTE SHEET (Rule 26) (RO/AU)

# Figure 2 (Continued)

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	-35	B-U	B-M
-5	SCCGCCGCG GTCCCCGCGGA CCCTCCAGAA GAGCGCCCGG CGCCGTGACT CAGCACTGGG GCGGAGCGGG GCGGACCAC -35	STIGGIGGGA GITIGIGGGA ITITITAGAA GAGIGGIIGG IGITGIGAIT IAGIAIIGGG GIGGAGIGGG GIGGGAITAI B-U	AGAA GAGCGGTCGG CGTCGTGATT TAGTATTGGG GCGGAGCGGG GCGGGATTAT B-M
9- L-	GCGGAGCGGG	GTGGAGTGGG	GCGGAGCGGG
	CAGCACTGGG	TAGTATTGGG	TAGTATTGGG
8161	CGCCGTGACT	TGTTGTGATT	CGTCGTGATT
-11 -10 -9 -8	GAGCGGCCGG	GAGTGGTTGG	GAGCGGTCGG
	CCCTCCAGAA	TTTTTAGAA	TTTTTAGAA
-13-12	GTCCGCGGGA	GTTTGTGGGA	STCGCCGGA GTTCGCGGGA TTTTTA
-15 -14	GCCGGCGGGA	GTTGGTGGGA	GTCGGCGGGA

CGPS-9 <GCCGCCCT CAARCRCCCT AAAAAATCTT CTC</p> CAA CAGCCRCCCT

B-U +46 B-M TCGCCGCCGC AGTCTTCGCC ACCAGTGAGT ACGCGCGGCC TIGITGITGI AGITTITGIT ATTAGIGAGI ATGIGGGIT ATTAGTGAGT ACGCGCGGTT . 0 TCGTCGTCGT AGTTTTCGTT CGCTGGAGTT TGTTGGAGTT CGTTGGAGTT GCGAGGCCTT GTGAGGTTTT GCGAGGTTTT CTCGGAGGCC TTTGGAGGTT TTCGGAGGTC က 4-TTTATAAGG CCTTATAAGG TTTATAGG

GCGAGGTTTT CGTTGGAGTT TCGTCGTC> CGPS-2 CGTT ATTAGTGAGT ACGCGCGGTT U CGPS-1

TTAA B-U CCAA +90 TTAA TAGTATGGGG TAGTATGGGG CAGCATGGGG TTAGAGTTTT TCAGAGCTCC TTAGAGTTTT CGCGICCCCG GGGAIGGGGC GGGATGGGGT GGGATGGGGT TGTGTTTTG CGCGTTTTCG 10 ത

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占 3+3 +++ +++ ‡ GST-Pi Gene ++++ ++++ ++++ ++++ ++++ ++++ +++ ++++ ++++ 344 XC ++ +++ +++ +++ ## 2+2 +++ ‡ +++ **+**+ ‡ +++ ‡ 8 ‡ ‡ ‡ ‡ + # + ‡ ‡ ‡ + + ‡ + + æ Ø the 2+3 ‡ ++ ‡ ‡ ‡ ‡ ‡ ‡ ‡ ‡ ‡ m ‡ ‡ # ‡ # ‡ # + ‡ + B + + + ü 3+3 ‡ ‡ # ‡ ‡ ‡ ‡ ‡ ‡ # ‡ ‡ ‡ + ‡ ‡ Д B + Sites 4+4 Methylation Status of Individual Z Z (NO/AU 2AN SUBSTITUTE SHEET (Rule **2**₹ ‡ ‡ # # ‡ ‡ ‡ ‡ ‡ + ++ ‡ ‡ ‡ ‡ ‡ m m 22 ≥ ‡ + # ‡ ‡ # ‡ ‡ + ++ ‡ + ++ ‡ ‡ + + + + + + + + <u>PG</u> ‡ ‡ ‡ # ‡ # ‡ # # # # # ‡ # # + + + 呂 ‡ ## ‡ ## ‡ ‡ ‡ ‡ ‡ ‡ ‡ ## ‡ ‡ ‡ ‡ ‡ ‡ Ľ 3A Figure SE 222 d, တ္

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# # ### ++++ **# +++** ## ++++ ++++ +++ +++ +++ + ‡ + + ## ‡ ### ++++ ‡ ‡‡ ++++ ‡ # **‡**‡‡ ‡ +++ ‡ ‡ ‡ ‡ |‡|‡|‡ # # # # | ‡ | m m m ┇ +++ ‡ # # ‡ ‡ + # # # | # | ‡ m m ‡ **‡** ‡ ‡ ++ В æ m m B + + æ æ Ø m ‡ ‡ ‡ ‡ ‡ ## ‡ # # ‡ B mm + B B m m m **m m m** + + ‡ ### ‡ ‡ # # # # 4 **P** മ + + + + + + ### +++ ‡ ### ‡ **‡** ‡ **‡** ## ‡ # ++++ ‡ ## ‡ ‡ ++++ ### ## ‡ ++++ ‡ +++ ### ‡ ## ‡

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Figure 3A (cont'd)

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_	_	++++	‡	‡	‡	4	###	‡		_		<del>+</del> ++	‡	‡	‡	+++	‡	‡	‡	_
_	_	4	4	<del>-</del> -	+	+	+	4		_	_	-	-	_	+	-	_	4	+	
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	1	1	<u> </u>			İ			1	1	1	1	1			1			#	
		8	3 8	3/5	3/5	3	16.	3/2				ě	28	i k	28	<u>رد</u>	3 5			200

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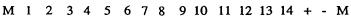
Heart 3 <u>∄∄∄∄</u> ‡ Pancreas 9 # # ‡ тапом Bone (5) #### **+** ### ‡ # Lung (5) ‡ ‡ # ## ‡ # Smooth muscle 9 ‡ ∄∄∄ ‡ Liver 9 ‡ ## Spleen 9 #### ‡ ## ‡ # # Brain 9 ‡ # # # Blood (13)##### ‡ ‡ ‡ ## ‡ ‡ <del>[</del> DC (10)## ŧIŧIŧ ##### ## #### ‡ ပ္ပ (4) 劃 <del>+++</del> ‡ 事事 |‡ # # # # # # BC 6 ∄∄∄∄ ### ‡ ‡ ‡ ‡ # ‡ # # LNCaP 6 #### 掛掛 ### ‡ # ### ‡ ## # PC-3 (10) ### # NormalP rostate (15) ‡ # # # # ‡ Site

Figure 3B Methylation Status of Individual Sites in the GST-Pi Gene

09/673448 PCT/AU99/00306 Received 30 June 1999

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FIGURE 3B (cont'd)





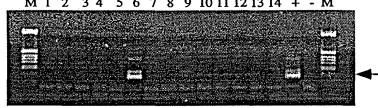


FIGURE 4A

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### Sample Number

1 2 3 4 5 6 7 8 9 10 Mncncncncncncncncnc+-





Sample	Tissue	Gleason	% Methylation Non CG rich PCR
1	Normal	N/A	_
	Cancer	3+3	4-4-4-
2	Normal	N/A	-
	Cancer	3+5	++
3	Normal	N/A	-
	Cancer	3+3	++
4	Normal	N/A	-
	Cancer	3+5	
5	Normal	N/A	_
	Cancer	2+2	++
6	Normal	N/A	_
	Cancer	3+3	
7	Normal	N/A	-
	Cancer	2+3	++
8	Normal	N/A	-
	Cancer	3+3	+-+
9	Normal	N/A	_
	Cancer	2+3	<del>-1-1-1-1</del> -
10	Normal	N/A	_
· <del>-</del>	Cancer	?	++

FIGURE 4B

B
M 1 2 3 4 5 6 7 8 9 + -

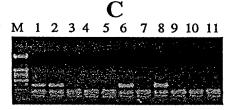
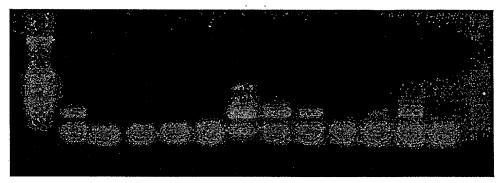
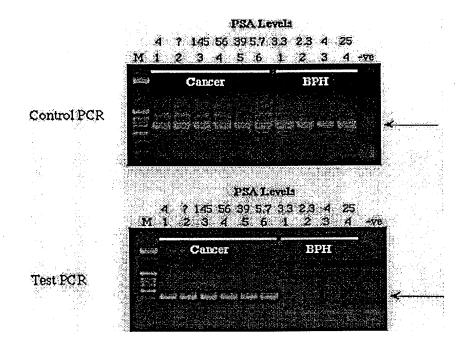


FIGURE 4C

#### M L D PNN C C C N N N -



# Figure 6



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## Figure 7A

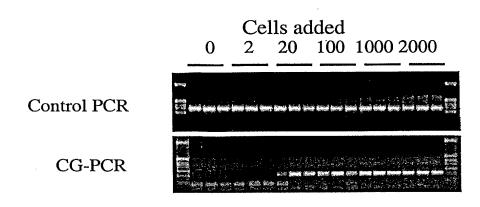
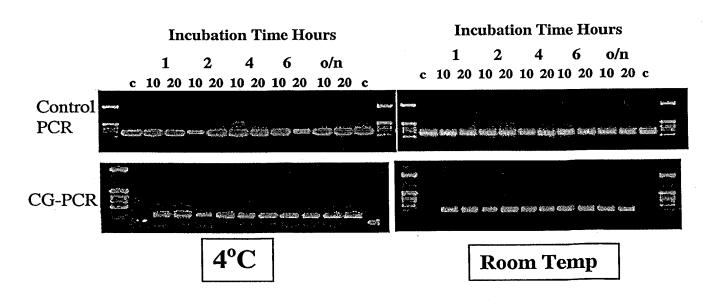


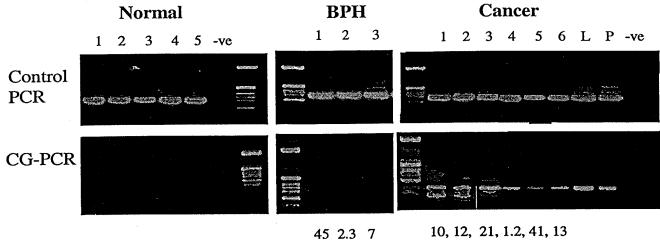
Figure 7B



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## Figure 8



**PSA Level** 

# Figure 9

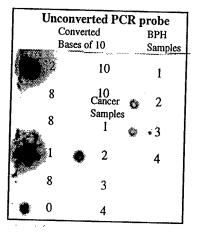
#### **Liver Cancer Tissue DNA extracts**



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Figure 10

Test Oligo's



	Con	verted PCR	probe
ĺ	C	onverted	BPH
ĺ	В	ases of 10	Samples
	2	<b>a</b> 10	<b>3</b> : 1
	8	10 ancer	2
,	8	Samples 1	3
**	1	2	4
	8	3	
*	0	4	

**Control Oligo** 

		BPH -Samples
2	10	1
8	Cancer	2
8	Samples 1	3
1	2	4
8	3	
0	4	
	2 8 8	8 10 Cancer Samples 1 1 2